

PB



PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,334

DATE: 02/14/2002

TIME: 15:11:47

Input Set : A:\6523-020-999.txt

Output Set: N:\CRF3\02142002\I763334.raw

P.5

4 <110> APPLICANT: Yale University  
 6 <120> TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER AND PITUITARY  
 7 DISORDERS WITH LATS PROTEINS, DERIVATIVES AND  
 8 FRAGMENTS, AND LATS KNOCK-OUT ANIMAL MODELS  
 10 <130> FILE REFERENCE: 6523-020-999  
 12 <140> CURRENT APPLICATION NUMBER: 09/763,334  
 C--> 13 <141> CURRENT FILING DATE: 1999-08-18  
 15 <160> NUMBER OF SEQ ID NOS: 9  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 3984  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (231)..(3620)  
 28 <400> SEQUENCE: 1  
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 33 acagtcctgg ggacttcctt gaaggatcat tttaactttt gctcagaaga aagctctgga 180  
 35 tctatcaaat aaagaagtcc ttctgtggg ctacatatat agatgttttc atg aag 236  
 36 Met Lys  
 37 1  
 39 agg agt gaa aag cca gaa gga tat aga caa atg agg cct aag acc ttt 284  
 40 Arg Ser Glu Lys Pro Glu Gly Tyr Arg Gln Met Arg Pro Lys Thr Phe  
 41 5 10 15  
 43 cct gcc agt aac tat act gtc agt agc cgg caa atg tta caa gaa att 332  
 44 Pro Ala Ser Asn Tyr Thr Val Ser Ser Arg Gln Met Leu Gln Glu Ile  
 45 20 25 30  
 47 cgg gaa tcc ctt agg aat tta tct aaa cca tct gat gct gct aag gct 380  
 48 Arg Glu Ser Leu Arg Asn Leu Ser Lys Pro Ser Asp Ala Ala Lys Ala  
 49 35 40 45 50  
 51 gag cat aac atg agt aaa atg tca acc gaa gat cct cga caa gtc aga 428  
 52 Glu His Asn Met Ser Lys Met Ser Thr Glu Asp Pro Arg Gln Val Arg  
 53 55 60 65  
 55 aat cca ccc aaa ttt ggg acg cat cat aaa gcc ttg cag gaa att cga 476  
 56 Asn Pro Pro Lys Phe Gly Thr His His Lys Ala Leu Gln Glu Ile Arg  
 57 70 75 80  
 59 aac tct ctg ctt cca ttt gca aat gaa aca aat tct tct cgg agt act 524  
 60 Asn Ser Leu Leu Pro Phe Ala Asn Glu Thr Asn Ser Ser Arg Ser Thr  
 61 85 90 95  
 63 tca gaa gtt aat cca caa atg ctt caa gac ttg caa gct gct gga ttt 572  
 64 Ser Glu Val Asn Pro Gln Met Leu Gln Asp Leu Gln Ala Ala Gly Phe

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65      100      105      110
67 gat gag gat atg gtt ata caa gct ctt cag aaa act aac aac aga agt 620
68 Asp Glu Asp Met Val Ile Gln Ala Leu Gln Lys Thr Asn Asn Arg Ser
69 115      120      125      130
71 ata gaa gca gca att gaa ttc att agt aaa atg agt tac caa gat cct 668
72 Ile Glu Ala Ala Ile Glu Phe Ile Ser Lys Met Ser Tyr Gln Asp Pro
73      135      140      145
75 cga cga gag cag atg gct gca gca gct gcc aga cct att aat gcc agc 716
76 Arg Arg Glu Gln Met Ala Ala Ala Ala Ala Arg Pro Ile Asn Ala Ser
77      150      155      160
79 atg aaa cca ggg aat gtg cag caa tca gtt aac cgc aaa cag agc tgg 764
80 Met Lys Pro Gly Asn Val Gln Gln Ser Val Asn Arg Lys Gln Ser Trp
81      165      170      175
83 aaa ggt tct aaa gaa tcc tta gtt cct cag agg cat ggc ccg cca cta 812
84 Lys Gly Ser Lys Glu Ser Leu Val Pro Gln Arg His Gly Pro Pro Leu
85      180      185      190
87 gga gaa agt gtg gcc tat cat tct gag agt ccc aac tca cag aca gat 860
88 Gly Glu Ser Val Ala Tyr His Ser Glu Ser Pro Asn Ser Gln Thr Asp
89 195      200      205      210
91 gta gga aga cct ttg tct gga tct ggt ata tca gca ttt gtt caa gct 908
92 Val Gly Arg Pro Leu Ser Gly Ser Gly Ile Ser Ala Phe Val Gln Ala
93      215      220      225
95 cac cct agc aac gga cag aga gtg aac ccc cca cca cca cct caa gta 956
96 His Pro Ser Asn Gly Gln Arg Val Asn Pro Pro Pro Pro Pro Gln Val
97      230      235      240
99 agg agt gtt act cct cca cca cct cca aga ggc cag act ccc cct cca 1004
100 Arg Ser Val Thr Pro Pro Pro Pro Pro Arg Gly Gln Thr Pro Pro Pro
101      245      250      255
103 aga ggt aca act cca cct ccc cct tca tgg gaa cca aac tct caa aca 1052
104 Arg Gly Thr Thr Pro Pro Pro Pro Ser Trp Glu Pro Asn Ser Gln Thr
105      260      265      270
107 aag cgc tat tct gga aac atg gaa tac gta atc tcc cga atc tct cct 1100
108 Lys Arg Tyr Ser Gly Asn Met Glu Tyr Val Ile Ser Arg Ile Ser Pro
109 275      280      285      290
111 gtc cca cct ggg gca tgg caa gag ggc tat cct cca cca cct ctc aac 1148
112 Val Pro Pro Gly Ala Trp Gln Glu Gly Tyr Pro Pro Pro Pro Leu Asn
113      295      300      305
115 act tcc ccc atg aat cct cct aat caa gga cag aga ggc att agt tct 1196
116 Thr Ser Pro Met Asn Pro Pro Asn Gln Gly Gln Arg Gly Ile Ser Ser
117      310      315      320
119 gtt cct gtt ggc aga caa cca atc atc atg cag agt tct agc aaa ttt 1244
120 Val Pro Val Gly Arg Gln Pro Ile Ile Met Gln Ser Ser Ser Lys Phe
121      325      330      335
123 aac ttt cca tca ggg aga cct gga atg cag aat ggt act gga caa act 1292
124 Asn Phe Pro Ser Gly Arg Pro Gly Met Gln Asn Gly Thr Gly Gln Thr
125      340      345      350
127 gat ttc atg ata cac caa aat gtt gtc cct gct ggc act gtg aat cgg 1340
128 Asp Phe Met Ile His Gln Asn Val Val Pro Ala Gly Thr Val Asn Arg
129 355      360      365      370

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131	cag	cca	cca	cct	cca	tat	cct	ctg	aca	gca	gct	aat	gga	caa	agc	cct	1388
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133				375					380					385			
135	tct	gct	tta	caa	aca	ggg	gga	tct	gct	gct	cct	tcg	tca	tat	aca	aat	1436
136	Ser	Ala	Leu	Gln	Thr	Gly	Gly	Ser	Ala	Ala	Pro	Ser	Ser	Tyr	Thr	Asn	
137				390					395					400			
139	gga	agt	att	cct	cag	tct	atg	atg	gtg	cca	aac	aga	aat	agt	cat	aac	1484
140	Gly	Ser	Ile	Pro	Gln	Ser	Met	Met	Val	Pro	Asn	Arg	Asn	Ser	His	Asn	
141				405					410					415			
143	atg	gaa	cta	tat	aac	att	agt	gta	cct	gga	ctg	caa	aca	aat	tgg	cct	1532
144	Met	Glu	Leu	Tyr	Asn	Ile	Ser	Val	Pro	Gly	Leu	Gln	Thr	Asn	Trp	Pro	
145				420					425					430			
147	cag	tca	tct	tct	gct	cca	gcc	cag	tca	tcc	ccg	agc	agt	ggg	cat	gaa	1580
148	Gln	Ser	Ser	Ser	Ala	Pro	Ala	Gln	Ser	Ser	Pro	Ser	Ser	Gly	His	Glu	
149	435								440					445		450	
151	atc	cct	aca	tgg	caa	cct	aac	ata	cca	gtg	agg	tca	aat	tct	ttt	aat	1628
152	Ile	Pro	Thr	Trp	Gln	Pro	Asn	Ile	Pro	Val	Arg	Ser	Asn	Ser	Phe	Asn	
153				455					460						465		
155	aac	cca	tta	gga	aat	aga	gca	agt	cac	tct	gct	aat	tct	cag	cct	tct	1676
156	Asn	Pro	Leu	Gly	Asn	Arg	Ala	Ser	His	Ser	Ala	Asn	Ser	Gln	Pro	Ser	
157				470					475					480			
159	gct	aca	aca	gtc	act	gca	att	aca	cca	gct	cct	att	caa	cag	cct	gtg	1724
160	Ala	Thr	Thr	Val	Thr	Ala	Ile	Thr	Pro	Ala	Pro	Ile	Gln	Gln	Pro	Val	
161				485					490					495			
163	aaa	agt	atg	cgt	gta	tta	aaa	cca	gag	cta	cag	act	gct	tta	gca	cct	1772
164	Lys	Ser	Met	Arg	Val	Leu	Lys	Pro	Glu	Leu	Gln	Thr	Ala	Leu	Ala	Pro	
165				500					505					510			
167	aca	cac	cct	tct	tgg	ata	cca	cag	cca	att	caa	act	gtt	caa	ccc	agt	1820
168	Thr	His	Pro	Ser	Trp	Ile	Pro	Gln	Pro	Ile	Gln	Thr	Val	Gln	Pro	Ser	
169	515								520					525		530	
171	cct	ttt	cct	gag	gga	acc	gct	tca	aat	gtg	act	gtg	atg	cca	cct	gtt	1868
172	Pro	Phe	Pro	Glu	Gly	Thr	Ala	Ser	Asn	Val	Thr	Val	Met	Pro	Pro	Val	
173				535					540					545			
175	gct	gaa	gct	cca	aac	tat	caa	gga	cca	cca	cca	ccc	tac	cca	aaa	cat	1916
176	Ala	Glu	Ala	Pro	Asn	Tyr	Gln	Gly	Pro	Pro	Pro	Pro	Tyr	Pro	Lys	His	
177				550					555					560			
179	ctg	ctg	cac	caa	aac	cca	tct	gtt	cct	cca	tac	gag	tca	atc	agt	aag	1964
180	Leu	Leu	His	Gln	Asn	Pro	Ser	Val	Pro	Pro	Tyr	Glu	Ser	Ile	Ser	Lys	
181				565					570					575			
183	cct	agc	aaa	gag	gat	cag	cca	agc	ttg	ccc	aag	gaa	gat	gag	agt	gaa	2012
184	Pro	Ser	Lys	Glu	Asp	Gln	Pro	Ser	Leu	Pro	Lys	Glu	Asp	Glu	Ser	Glu	
185				580					585					590			
187	aag	agt	tat	gaa	aat	gtt	gat	agt	ggg	gat	aaa	gaa	aag	aaa	cag	att	2060
188	Lys	Ser	Tyr	Glu	Asn	Val	Asp	Ser	Gly	Asp	Lys	Glu	Lys	Lys	Gln	Ile	
189	595								600					605		610	
191	aca	act	tca	cct	att	act	gtt	agg	aaa	aac	aag	aaa	gat	gaa	gag	cga	2108
192	Thr	Thr	Ser	Pro	Ile	Thr	Val	Arg	Lys	Asn	Lys	Lys	Asp	Glu	Glu	Arg	
193				615					620					625			
195	agg	gaa	tct	cgt	att	caa	agt	tat	tct	cct	caa	gca	ttt	aaa	ttc	ttt	2156

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196	Arg	Glu	Ser	Arg	Ile	Gln	Ser	Tyr	Ser	Pro	Gln	Ala	Phe	Lys	Phe	Phe	
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200	Met	Glu	Gln	His	Val	Glu	Asn	Val	Leu	Lys	Ser	His	Gln	Gln	Arg	Leu	
201			645					650					655				
203	cat	cgt	aaa	aaa	caa	tta	gag	aat	gaa	atg	atg	cgg	ggt	gga	tta	tct	2252
204	His	Arg	Lys	Lys	Gln	Leu	Glu	Asn	Glu	Met	Met	Arg	Val	Gly	Leu	Ser	
205		660					665					670					
207	caa	gat	gcc	cag	gat	caa	atg	aga	aag	atg	ctt	tgc	caa	aaa	gaa	tct	2300
208	Gln	Asp	Ala	Gln	Asp	Gln	Met	Arg	Lys	Met	Leu	Cys	Gln	Lys	Glu	Ser	
209	675					680					685				690		
211	aat	tac	atc	cgt	ctt	aaa	agg	gct	aaa	atg	gac	aag	tct	atg	ttt	gtg	2348
212	Asn	Tyr	Ile	Arg	Leu	Lys	Arg	Ala	Lys	Met	Asp	Lys	Ser	Met	Phe	Val	
213					695				700					705			
215	aag	ata	aag	aca	cta	gga	ata	gga	gca	ttt	ggt	gaa	gtc	tgt	cta	gca	2396
216	Lys	Ile	Lys	Thr	Leu	Gly	Ile	Gly	Ala	Phe	Gly	Glu	Val	Cys	Leu	Ala	
217				710					715				720				
219	aga	aaa	gta	gat	act	aag	gct	ttg	tat	gca	aca	aaa	act	ctt	cga	aag	2444
220	Arg	Lys	Val	Asp	Thr	Lys	Ala	Leu	Tyr	Ala	Thr	Lys	Thr	Leu	Arg	Lys	
221			725				730					735					
223	aaa	gat	ggt	ctt	ctt	cga	aat	caa	gtc	gct	cat	ggt	aag	gct	gag	aga	2492
224	Lys	Asp	Val	Leu	Leu	Arg	Asn	Gln	Val	Ala	His	Val	Lys	Ala	Glu	Arg	
225		740					745					750					
227	gat	atc	ctg	gct	gaa	gct	gac	aat	gaa	tgg	gta	ggt	cgt	cta	tat	tat	2540
228	Asp	Ile	Leu	Ala	Glu	Ala	Asp	Asn	Glu	Trp	Val	Val	Arg	Leu	Tyr	Tyr	
229	755				760					765					770		
231	tca	ttc	caa	gat	aag	gac	aat	tta	tac	ttt	gta	atg	gac	tac	att	cct	2588
232	Ser	Phe	Gln	Asp	Lys	Asp	Asn	Leu	Tyr	Phe	Val	Met	Asp	Tyr	Ile	Pro	
233				775					780					785			
235	ggg	ggt	gat	atg	atg	agc	cta	tta	att	aga	atg	ggc	atc	ttt	cca	gaa	2636
236	Gly	Gly	Asp	Met	Met	Ser	Leu	Leu	Ile	Arg	Met	Gly	Ile	Phe	Pro	Glu	
237				790					795				800				
239	agt	ctg	gca	cga	ttc	tac	ata	gca	gaa	ctt	acc	tgt	gca	ggt	gaa	agt	2684
240	Ser	Leu	Ala	Arg	Phe	Tyr	Ile	Ala	Glu	Leu	Thr	Cys	Ala	Val	Glu	Ser	
241			805					810					815				
243	ggt	cat	aaa	atg	ggt	ttt	att	cat	aga	gat	att	aaa	cct	gat	aat	att	2732
244	Val	His	Lys	Met	Gly	Phe	Ile	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Ile	
245		820					825					830					
247	ttg	att	gat	cgt	gat	ggt	cat	att	aaa	ttg	act	gac	ttt	ggc	ctc	tgc	2780
248	Leu	Ile	Asp	Arg	Asp	Gly	His	Ile	Lys	Leu	Thr	Asp	Phe	Gly	Leu	Cys	
249	835				840					845					850		
251	act	ggc	ttc	aga	tgg	aca	cac	gat	tct	aag	tac	tat	cag	agt	ggt	gac	2828
252	Thr	Gly	Phe	Arg	Trp	Thr	His	Asp	Ser	Lys	Tyr	Tyr	Gln	Ser	Gly	Asp	
253				855					860						865		
255	cat	cca	cgg	caa	gat	agc	atg	gat	ttc	agt	aat	gaa	tgg	ggg	gat	ccc	2876
256	His	Pro	Arg	Gln	Asp	Ser	Met	Asp	Phe	Ser	Asn	Glu	Trp	Gly	Asp	Pro	
257			870					875					880				
259	tca	agc	tgt	cga	tgt	gga	gac	aga	ctg	aag	cca	tta	gag	cgg	aga	gct	2924
260	Ser	Ser	Cys	Arg	Cys	Gly	Asp	Arg	Leu	Lys	Pro	Leu	Glu	Arg	Arg	Ala	

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261      885      890      895
263 gca cgc cag cac cag cga tgt cta gca cat tct ttg gtt ggg act ccc 2972
264 Ala Arg Gln His Gln Arg Cys Leu Ala His Ser Leu Val Gly Thr Pro
265      900      905      910
267 aat tat att gca cct gaa gtg ttg cta cga aca gga tac aca cag ttg 3020
268 Asn Tyr Ile Ala Pro Glu Val Leu Leu Arg Thr Gly Tyr Thr Gln Leu
269 915      920      925      930
271 tgt gat tgg tgg agt gtt ggt gtt att ctt ttt gaa atg ttg gtg gga 3068
272 Cys Asp Trp Trp Ser Val Gly Val Ile Leu Phe Glu Met Leu Val Gly
273      935      940      945
275 caa cct cct ttc ttg gca caa aca cca tta gaa aca caa atg aag gtt 3116
276 Gln Pro Pro Phe Leu Ala Gln Thr Pro Leu Glu Thr Gln Met Lys Val
277      950      955      960
279 atc aac tgg caa aca tct ctt cac att cca cca caa gct aaa ctc agt 3164
280 Ile Asn Trp Gln Thr Ser Leu His Ile Pro Pro Gln Ala Lys Leu Ser
281      965      970      975
283 cct gaa gct tct gat ctt att att aaa ctt tgc cga gga ccc gaa gat 3212
284 Pro Glu Ala Ser Asp Leu Ile Ile Lys Leu Cys Arg Gly Pro Glu Asp
285      980      985      990
287 cgc tta ggc aag aat ggt gct gat gaa ata aaa gct cat cca ttt ttt 3260
288 Arg Leu Gly Lys Asn Gly Ala Asp Glu Ile Lys Ala His Pro Phe Phe
289 995      1000      1005      1010
291 aaa aca att gac ttc tcc agt gac ctg aga cag cag tct gct tca tac 3308
292 Lys Thr Ile Asp Phe Ser Ser Asp Leu Arg Gln Gln Ser Ala Ser Tyr
293      1015      1020      1025
295 att cct aaa atc aca cac cca aca gat aca tca aat ttt gat cct gtt 3356
296 Ile Pro Lys Ile Thr His Pro Thr Asp Thr Ser Asn Phe Asp Pro Val
297      1030      1035      1040
299 gat cct gat aaa tta tgg agt gat gat aac gag gaa gaa aat gta aat 3404
300 Asp Pro Asp Lys Leu Trp Ser Asp Asp Asn Glu Glu Glu Asn Val Asn
301      1045      1050      1055
303 gac act ctc aat gga tgg tat aaa aat gga aag cat cct gaa cat gca 3452
304 Asp Thr Leu Asn Gly Trp Tyr Lys Asn Gly Lys His Pro Glu His Ala
305      1060      1065      1070
307 ttc tat gaa ttt acc ttc cga agg ttt ttt gat gac aat ggc tac cca 3500
308 Phe Tyr Glu Phe Thr Phe Arg Arg Phe Phe Asp Asn Gly Tyr Pro
309 1075      1080      1085      1090
311 tat aat tat ccg aag cct att gaa tat gaa tac att aat tca caa ggc 3548
312 Tyr Asn Tyr Pro Lys Pro Ile Glu Tyr Glu Tyr Ile Asn Ser Gln Gly
313      1095      1100      1105
315 tca gag cag cag tcg gat gaa gat gat caa aac aca ggc tca gag att 3596
316 Ser Glu Gln Gln Ser Asp Glu Asp Asp Gln Asn Thr Gly Ser Glu Ile
317      1110      1115      1120
319 aaa aat cgc gat cta gta tat gtt taacacacta gtaaataaat gtaatgagga 3650
320 Lys Asn Arg Asp Leu Val Tyr Val
321      1125      1130
323 tttgtaaaag ggccctgaaat gcgaggtgtt ttgaggttct gagagtaaaa ttatgcaaat 3710
325 atgacagagc tatatatgtg tgctctgtgt acaatatattt attttcctaa attatgggaa 3770
327 atccttttaa aatgttaatt tattccagcc gtttaaataca gtatttagaa aaaaattggt 3830

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Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.



## VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:2000 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8